

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 15, 2001, 11:10:52 ; Search time 47.29 Seconds
(without alignments)
34.699 Million cell updates/sec

Title: US-09-288-719-2

Perfect score: 75

Sequence: 1 GGGSGGSGRASGGGS 14

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	65	86.7	493	4	Q14720
2	64	85.3	738	5	002402
3	63	84.0	162	10	Q9M0B4
4	62	82.7	190	13	Q9PVG4
5	62	82.7	699	11	Q9Z0Y5
6	62	82.7	699	11	Q9QY47
7	62	82.7	751	11	Q9R218
8	62	82.7	751	11	Q9YR22
9	61	81.3	102	10	Q23369
10	60	80.0	278	10	Q9L732
11	60	80.0	290	4	Q9UR32
12	60	80.0	291	4	Q14621
13	60	80.0	298	11	Q9QYF0
14	60	80.0	306	4	Q9UKM9
15	60	80.0	378	5	Q76736
16	60	80.0	509	5	Q96754
17	60	80.0	542	5	Q9W0K7
18	60	80.0	592	2	Q9PF60
19	60	80.0	944	5	Q9VK59

20	60	80.0	979	5	Q9Q1H7	Q9U1H7 drosophila
21	60	80.0	1433	11	Q07563	Q07563 mus musculu
22	59	78.7	96	5	Q9YKS2	Q9YKS2 drosophila
23	59	78.7	130	5	Q9YXD8	Q9YXD8 drosophila
24	59	78.7	133	10	Q9LH30	Q9LH30 oryza sativ
25	59	78.7	136	5	Q18444	Q18444 caenorhabd
26	59	78.7	150	10	Q80490	Q80490 arabidopsis
27	59	78.7	175	10	Q9LSN6	Q9LSN6 arabidopsis
28	59	78.7	191	5	Q46029	Q46029 chironomus
29	59	78.7	221	10	Q65514	Q65514 arabidopsis
30	59	78.7	251	10	Q9SND4	Q9SND4 oryza sativ
31	59	78.7	291	10	Q39337	Q39337 brassica na
32	59	78.7	301	5	Q15647	Q15647 plasmodium
33	59	78.7	316	5	Q19111	Q19111 caenorhabd
34	59	78.7	318	10	Q38777	Q38777 allium sati
35	59	78.7	344	13	Q42403	Q42403 gallus gall
36	59	78.7	382	5	Q9VPE1	Q9VPE1 drosophila
37	59	78.7	451	4	Q9NXD2	Q9NXD2 hmo sapien
38	59	78.7	529	5	Q9VK03	Q9VK03 drosophila
39	59	78.7	561	4	Q14664	Q14664 hmo sapien
40	58	77.3	160	10	Q9SMA8	Q9SMA8 glycine max
41	58	77.3	201	4	Q75946	Q75946 hmo sapien
42	58	77.3	218	4	Q60682	Q60682 hmo sapien
43	58	77.3	267	5	Q9VZ13	Q9VZ13 drosophila
44	58	77.3	319	10	Q9L7F4	Q9L7F4 oryza sativ
45	58	77.3	435	5	Q01663	Q01663 caenorhabd

ALIGNMENTS

RESULT 1
ID Q14720 PRELIMINARY: PRT: 493 AA.
AC Q14720;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DI 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE EPIDERMAL 67-KDA TYPE II KERATIN MRNA (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-85207740; PubMed-2581964;
RA Steinert P.M., Parry D.A.D., Idler W.W., Johnson L.D., Steven A.C.,
RA Koop D.R.;
RT "Amino acid sequences of mouse and human epidermal type II keratins of
RT Mr 67,000 provide a systematic basis for the structural and functional
RT diversity of the end domains of keratin intermediate filament
RT subunits".
RL J. Biol. Chem. 260:7142-7149(1985).
CC -; SIMILARITY: TO ALL OTHER INTERMEDIATE FILAMENT PROTEINS.
CC EMBL: M10938; AAA36153.1; -;
DR INTERPRO: IPR001664; -;
DR INTERPRO: IPR003054; -;
DR PFAM: PF00038; filament. 1.
DR PRINTS: PR01276; TYPE2KERATIN.
DR PROSITE: PS00226; IF. 1.
KW Keratin; Intermediate filament; Coiled coil; Heptad repeat pattern.
FT NON_TER
SQ SEQUENCE 493 AA: 52788 MW; E764DC56DD988AC9 CRC64;

Query Match 86.7%; Score 65; DB 4; Length 493;
Best Local Similarity 85.7%; Pred. No. 0.56;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 1 GGGSGGSGRASGGGS 14
Db 444 GGGSGGSGRASGGGS 457

RESULT 2
002402 PRELIMINARY: PRT: 738 AA.
AC 002402;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE INSOLUBLE PROTEIN.
OS Pinctada fucata.
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pterioida;
OC Pterioidea; Pteridae; Pinctada.
OX NCBI_TaxID=50425;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97320490; PubMed=9177341;
RA Sudo S., Fujikawa T., Nakagura T., Ohkubo T., Sakaguchi K., Tanaka M.,
RA Nakashima K., Takahashi T.;
RT "Structures of mollusc shell framework proteins."
RL Nature 387:563-564(1997).
DR EMBL; D86074; BAA20466.1; -;
SQ SEQUENCE 738 AA; 61723 MW; PDP984139BF3BA59 CRC64;

Query Match 85.3%; Score 64; DB 5; Length 738;
Best Local Similarity 85.7%; Pred. No. 1.1;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGGSGGGRASGGGS 14
Db 671 GGGSGGGRASGGGS 684

RESULT 3
Q9MOB4 PRELIMINARY: PRT: 162 AA.
AC Q9MOB4;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE GLYCINE-RICH PROTEIN.
GN AT4G30460.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicaceae; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Lamar B., Stoneking T., Stumpf J., Mewes H.W., Lemcke K.,
RA Meyer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL161577; CAB79764.1; -;
SQ SEQUENCE 162 AA; 13738 MW; 4D09D2210AF6F0C7 CRC64;

Query Match 84.0%; Score 63; DB 10; Length 162;
Best Local Similarity 78.6%; Pred. No. 0.32;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGSGGGRASGGGS 14
Db 128 GGGSGGGRASGGGS 141

RESULT 4
Q9PVG4 PRELIMINARY: PRT: 190 AA.
ID Q9PVG4
AC Q9PVG4;

DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE TWIST.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Isaac A., Cohn M., Patel K., Atalloris A., Spicer D.B., Cooke J.,
RA Tickle C.;
RT "Snail" transcription factors and wing determination: a new example
of conservation between vertebrate and insect development."
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF093816; AAF00072.1; -;
DR HSSP; P10085; IMDY.
DR INTERPRO; IPR001092; -;
DR INTERPRO; IPR003015; -;
DR PFAM; PF00010; HLH; 1.
DR PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN; 1.
SQ SEQUENCE 190 AA; 20403 MW; 5B74A243F256CDFD CRC64;

Query Match 82.7%; Score 62; DB 13; Length 190;
Best Local Similarity 78.6%; Pred. No. 0.51;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGSGGGRASGGGS 14
Db 74 GGGSGGGRASGGGS 87

RESULT 5
Q9Z0Y5 PRELIMINARY: PRT: 699 AA.
AC Q9Z0Y5;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TReMBLrel. 10, Last annotation update)
DE DACHSHUND VARIANT 2.
GN DACH.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LIMB BUD;
RX MEDLINE=99112783; PubMed=9915577;
RA Caubit X., Thangarajah R., Thell T., Wirth J., Nothwang H.G.,
RA Ruther U., Kraus S.;
RT "Mouse Dac, a novel nuclear factor with homology to Drosophila
dachshund shows a dynamic expression in the neural crest, the eye, the
RT neocortex, and the limb bud."
RL Dev. Dyn. 214:66-80(1999).
DR EMBL; AF090437; AAD16098.1; -;
SQ SEQUENCE 699 AA; 72609 MW; 2F6B77D48200A319 CRC64;

Query Match 82.7%; Score 62; DB 11; Length 699;
Best Local Similarity 78.6%; Pred. No. 1.9;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGSGGGRASGGGS 14
Db 84 GGGSGGGRASGGGS 97

RESULT 6
Q9QY47 PRELIMINARY: PRT: 699 AA.
ID Q9QY47

AC Q90Y47;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE DACH PROTEIN.
 GN DACH.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99432380; PubMed=10502109;
 RA Davis R.J., Shen W., Heanne T.A., Mardon G.;
 RT "Mouse DACH, a homologue of Drosophila dachshund, is expressed in the
 RL developing retina, brain and limbs.";
 DR Dev. Genes Evol. 209:526-536(1999).
 SQ SEQUENCE 699 AA; 72533 MW; 912197D66E4B29A CRC64;

Query Match 82.7%; Score 62; DB 11; Length 699;
 Best Local Similarity 78.6%; Pred. No. 1.9;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GGGSGGGRASGGS 14
 DB 84 GGGSGGNGGGGGS 97

RESULT 7
 ID 09R218 PRELIMINARY; PRT; 751 AA.
 AC 09R218;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE DACHSHUND VARIANT 1.
 GN DACH.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE-LIMB BUD;
 MEDLINE=99112783; PubMed=9915577;
 RA Caubit X., Thangarajah R., Theil T., Wirth J., Nottwang H.G.,
 RA Ruther U., Krauss S.;
 RT "Mouse Dac, a novel nuclear factor with homology to Drosophila
 RT dachshund shows a dynamic expression in the neural crest, the eye, the
 RL neocortex, and the limb bud.";
 DR Dev. Dyn. 214:66-80(1999).
 EMBL: AF090436; AAD16097.1;
 SQ SEQUENCE 751 AA; 78047 MW; AF55AF743BF2B2C1 CRC64;

Query Match 82.7%; Score 62; DB 11; Length 751;
 Best Local Similarity 78.6%; Pred. No. 2;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GGGSGGGRASGGS 14
 DB 84 GGGSGGNGGGGGS 97

RESULT 8
 ID 090YB2 PRELIMINARY; PRT; 751 AA.
 AC 090YB2;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)

DE DACHSHUND.
 GN DACH.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99432381; PubMed=10502110;
 RA Kozmik Z., Pfeiffer P., Kralova J., Paces J., Paces V., Kalousova A.,
 RA Cvek A.;
 RT "Molecular cloning and expression of the human and mouse homologues of
 RT the Drosophila dachshund gene.";
 RL Dev. Genes Evol. 209:537-545(1999).
 DR EMBL: AF102547; AAF04742.1;
 SQ SEQUENCE 751 AA; 77971 MW; 0679337DBA742BC9 CRC64;

Query Match 82.7%; Score 62; DB 11; Length 751;
 Best Local Similarity 78.6%; Pred. No. 2;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GGGSGGGRASGGS 14
 DB 84 GGGSGGNGGGGGS 97

RESULT 9
 ID 023369 PRELIMINARY; PRT; 102 AA.
 AC 023369;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE HYPOTHETICAL 9.8 KDA PROTEIN.
 GN AT4G15150.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bevan M., Stiekema W., Murphy G., Wambutt R., Pohl T., Terryn N.,
 RA Kreis M., Kavanagh T., Ertani K.D., Rieger M., James R.,
 RA Puidomenech P., Hatzopoulos P., Obermaier B., Dueserhoft A.,
 RA Jones J., Palme K., Anstorge W., Delseny M., Bancroft I., Mewes H.W.,
 RA Schueiller C., Chaiwalits N.;
 RL submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Z97338; CAB10294.1;
 DR EMBL: AL161540; CAB78557.1;
 KW Hypothetical protein.
 SQ SEQUENCE 102 AA; 9783 MW; 5821266ABE975A9F CRC64;

Query Match 81.3%; Score 61; DB 10; Length 102;
 Best Local Similarity 78.6%; Pred. No. 0.36;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GGGSGGGRASGGS 14
 DB 50 GGGSGGNGGGGGS 63

RESULT 10
 ID 09LT32 PRELIMINARY; PRT; 278 AA.
 AC 09LT32;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)

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DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, last annotation update)
OS GENOMIC DNA, CHROMOSOME 3, PI CLONE: MOE17.
OC Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons: core eudicots: Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA;
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu F., Tabata S.;
RL Submitted (Apr-1999) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT clones."
RL DNA Res. 7:131-135(2000).
DR EMBL: AB025629; BAB02497.1;
SQ SEQUENCE 278 AA; 30182 MW; 5E12F3C8CC7D9D5D CRC64;

Query Match 80.0%; Score 60; DB 10; Length 278;
Best Local Similarity 78.6%; Pred. No. 1.3;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GGGGSGGRASGGG 14
Db 155 GGGGCGGRISGGSS 168

RESULT 11
OY0UE3 PRELIMINARY; PRT; 290 AA.
ID 090UE3;
AC 090UE3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, last annotation update)
DE D564K7.3 (AUTOANTIGEN P542).
GN D564K7.3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Carnivora; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Laird G.;
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AL011668; CAB43742.1;
DR INTERPRO: IPR000504;
DR PFM; PF00076; ttm; 1.
DR PROSITE: PS00030; RNP_1; UNKNOWN_1.
SQ SEQUENCE 290 AA; 30364 MW; 228F7E277DB066C9 CRC64;

Query Match 80.0%; Score 60; DB 4; Length 290;
Best Local Similarity 84.6%; Pred. No. 1.4;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGGGSGGRASGGG 13
Db 219 GGGGSGGGGGGGG 231

RESULT 12
OY04621 PRELIMINARY; PRT; 291 AA.
AC 014621;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1998 (TREMBLrel. 08, last sequence update)

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DT 01-OCT-2000 (TREMBLrel. 15, last annotation update)
DE AUTOANTIGEN P542.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Carnivora; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-95190029; PubMed-7533788;
RA Vaughan J.H., Valbrach J.R., Nguyen M.D., Handley H.H., Smith R.S.,
RA Patrick K., Rhodes G.H.;
RT "Epstein-Barr virus-induced autoimmune responses. I. Immunoglobulin M
RT autoantibodies to proteins mimicking and not mimicking Epstein-Barr
RT virus nuclear antigen-1."
RL J. Clin. Invest. 95:1306-1315(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-98018738; PubMed-9376072;
RA Rhodes G.H., Valbrach J.R., Nguyen M.-D., Vaughan J.H.;
RT "The p542 gene encodes an autoantigen that cross-reacts with EBNA-1 of
RT the Epstein Barr virus and which may be a heterogeneous nuclear
RT ribonucleoprotein."
RL J. Autoimmun. 10:447-454(1997).
RN [3]
RP SEQUENCE FROM N.A.
RA Vaughan J.;
RL Submitted (FEB-1995) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Vaughan J.;
RL Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: L38696; AAC28898.1;
DR INTERPRO: IPR000504;
DR PFM; PF00076; ttm; 1.
DR PROSITE: PS00030; RNP_1; UNKNOWN_1.
SQ SEQUENCE 291 AA; 30438 MW; F8DB4BE6DA08347F CRC64;

Query Match 80.0%; Score 60; DB 4; Length 291;
Best Local Similarity 84.6%; Pred. No. 1.4;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGGGSGGRASGGG 13
Db 220 GGGGSGGGGGGGG 232

RESULT 13
OY0YF0 PRELIMINARY; PRT; 298 AA.
ID 090YF0;
AC 090YF0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, last annotation update)
DE CN 8 scfv.
GN CN 8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE-SPLEEN;
RA Shinohara N., Demura T., Fukuda H.;
RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE-SPLEEN;
RA Shinohara N., Demura T., Fukuda H.;
RT "Isolation of a novel type of vascular cell wall-specific monoclonal
RT antibody recognizing a cell polarity using a phage display subtraction
RT method."
RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.

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DR EMBL: AB036341; BAA88633.1; -
 DR HSSP: F01607; 1REI.
 DR INTERPRO: IPR003006; -
 DR PFAM: PF00047; 197.2
 SQ SEQUENCE 298 AA; 31867 MW; E0F968BA17004317 CRC64;

Query Match
 Best Local Similarity 80.0%; Score 60; DB 11; Length 298;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGSGGRASGGG 13
 ||||| ||||
 DB 158 GGGGSGGGGGGGG 170

RESULT 14
 Q9UKM9 PRELIMINARY; PRT; 306 AA.

AC Q9UKM9:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, last annotation update)
 DE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN, ALTERNATE TRANSCRIPT.
 GN RALY.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBL_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TESTIS;
 RX MEDLINE=9431566; PubMed=10500250;
 RA Khrebtkova I., Kuklin A., Woychik R.P., Michaud E.J.;
 RT "Alternative processing of the human and mouse raly genes."
 RL Biochim. Biophys. Acta 1447:107-112(1999).
 DR EMBL: AF148457; AAF04487.1; -
 DR INTERPRO: IPR000504; -
 DR PFAM: PF00076; ITM; 1.
 DR PROSITE: PS00030; RNP_1; UNKNOWN_1.
 KM Nucleocapsid; Ribonucleoprotein.
 SQ SEQUENCE 306 AA; 32463 MW; 7FA376D3BD8E4728 CRC64;

Query Match
 Best Local Similarity 80.0%; Score 60; DB 4; Length 306;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGSGGRASGGG 13
 ||||| ||||
 DB 235 GGGGSGGGGGGGG 247

RESULT 15
 ID 076736 PRELIMINARY; PRT; 378 AA.
 AC 076736:
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, last annotation update)
 DE TIPB.
 GN TIPB.
 OS Dictyostellium discoideum (Slime mold).
 OC Eukaryota; Dictyostelida; Dictyostelium.
 OX NCBL_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX4;
 RA Stege J.T., Laub M.T., Loomis W.F.;
 RT "Interaction of tip genes in early Dictyostellium discoideum
 development."
 RL submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF079444; AAC31915.1; -

DR INTERPRO: IPR000276; -
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 SQ SEQUENCE 378 AA; 41217 MW; 3F67CE74BA8EC88E CRC64;

Query Match
 Best Local Similarity 80.0%; Score 60; DB 5; Length 378;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGSGGRASGGG 14
 ||||| ||||
 DB 186 GGGGSGGGGGGGG 199

Search completed: March 15, 2001, 11:10:54
 Job time: 1110 sec

